



SEQUENCE LISTING

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<120> MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS

<130> 53356-5001-US

<140> US 09/319,724

<141> 1999-09-08

<150> EP 96402719.7

<151> 1996-12-12

<150> PCT/EP97/07339

<151> 1997-12-12

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 439

<212> PRT

<213> Homo sapiens

<400> 1

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Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu Glu Ile
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Gly Phe Asn Gly Asn Arg Ile Val Asp Val Asn Leu Thr Ser Glu Gly
35 40 45

Lys Val Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val
50 55 60

Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr
65 70 75 80

Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe
85 90 95

Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile

100	105	110
Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu		
115	120	125
Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys		
130	135	140
Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe		
145	150	155
Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile		
165	170	175
Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser		
180	185	190
Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn		
195	200	205
Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp		
210	215	220
Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys		
225	230	235
Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser		
245	250	255
Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe		
260	265	270
Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn		
275	280	285
Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg		
290	295	300
Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys		
305	310	315
Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe		
325	330	335

Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe
 340 345 350

Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr
 355 360 365

Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln
 370 375 380

Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met
 385 390 395 400

Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe
 405 410 415

Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu
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Gly Ile Met Cys Gly Ala Ile
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<210> 2
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 <212> DNA
 <213> Homo sapiens

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 gatgttaatc taactagtga aggaaagggtg aaactgggttc caaatactaa aatccagatg 180
 tcatattcag taaaatggaa aaagtcagat gtgaaatttg aagatcgatt tgacaaatat 240
 cttgatccgt ctttttttca acatcggatt cattgggtttt caattttcaa ctccctcatg 300
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 tatggatgga aacagggtgca tggagatgta tttagaccat caagtcaccc actgatattt 480
 tcctctctga ttggttctgg atgtcagata tttgctgtgt ctctcatcgt tattattggt 540
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 tatgctgcta cgtctccagt gaatgggttat tttggaggaa gtctgtatgc tagacaagga 660

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gttggtacaa tacttggccg aaatctgtca ggtcagccca actttccttg tcgtgtcaat	900
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ttcatgatgg tgatcttctt ggtgggctta gtttcaatga ttttaatgag aacattaaga	180
aaagattatg ctcggtacag taaagaggaa gaaatggatg atatggatag agacctagga	240
gatgaatatg gatggaaaca ggtgcatgga gatgtattta gaccatcaag tcacccactg	300
atattttcct ctctgattgg ttctggatgt cagatatttg ctgtgtctct catcgttatt	360
attgttgcaa tgatagaaga tttatatact gagaggggat caatgctcag tacagccata	420
tttgtctatg ctgctacgtc tccagtgaat ggttatttta gaggaagtct gtatgctaga	480
caaggaggaa ggagatggat aaagcagatg tttattgggg cattccttat cccagctatg	540
gtgtgtggca ctgccttctt catcaatttc atagccattt attaccatgc ttcaagagcc	600
attccttttg gaacaatggg ggccgtttgt tgcactgtgt tttttgttat tcttcctcta	660
aatcttggtg gtacaatact tggccgaaat ctgtcaggtc agcccaactt tccttgctgt	720
gtcaatgctg tgccctgtcc tataccggag aaaaaatggg tcatggagcc tgcggttatt	780
gtttgcctgg gtggaatttt accttttggg tcaatcttta ttgaaatgta tttcatcttc	840

acgtctttct gggcatataa gatctattat gtctatggct tcatgatgct ggtgctgggt 900
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 gaaga 965

<210> 4
 <211> 285
 <212> DNA
 <213> Homo sapiens

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 ccgtcctttt ttcaacatcg gattcattgg ttttcaattt tcaactcctt catgatgggtg 120
 atcttcttgg tgggcttagt ttcaatgatt ttaatgagaa cattaagaaa agattatgct 180
 cggtagagta aagaggaaga aatggatgat atggatagag acctaggaga tgaatatgga 240
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<210> 5
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Fragment generated by acidic cleavage of polypeptide able to bind ICYP

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Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe Asn
 1 5 10 15

Ser

<210> 6
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Fragment generated by acidic cleavage of polypeptide able to bind ICYP

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa can be any amino acid

<400> 6

Asp Pro Xaa Phe Phe Gln His Arg Ile His Val Phe Ser Ile Phe Asn
1 5 10 15

His

<210> 7

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> probe/primer

<400> 7

tcagtaaaat ggaaaaagtc

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<210> 8

<211> 20

<212> DNA

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<220>

<223> probe/primer

<400> 8

tgggtgactt gatggtctaa

20

<210> 9

<211> 19

<212> DNA

<213> Artificial sequence

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<223> probe/primer

<400> 9

gctgtgtctc tcatcgta

19

<210> 10

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> probe/primer

<400> 10

ccatccatat tcatctccta

20

<210> 11
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 <220>
 <223> probe/primer

 <400> 11
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<210> 12
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 <212> DNA
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 <220>
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 <400> 12
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<210> 13
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 <213> Homo sapiens

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 <222> (3)..(1730)
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 1 5 10 15

 gac gag cac gaa cac acg tat caa gat aaa gag gaa gtt gtc tta tgg 95
 Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp
 20 25 30

 atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat aag tac 143
 Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr
 35 40 45

 ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt cat tac 191
 Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr
 50 55 60

 cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa ttt agt 239
 His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser
 65 70 75

 ggt ctg gat att aaa ttt aaa gat gat gtg atg cca gcc act tac tgt 287

Gly 80	Leu	Asp	Ile	Lys	Phe 85	Lys	Asp	Asp	Val	Met 90	Pro	Ala	Thr	Tyr	Cys 95	
gaa Glu	att Ile	gat Asp	tta Leu	gat Asp	aaa Lys	gaa Glu	aag Lys	aga Arg	gat Asp	gca Ala	ttt Phe	gta Val	tat Tyr	gcc Ala	ata Ile	335
				100					105					110		
aaa Lys	aat Asn	cat His	tac Tyr	tgg Trp	tac Tyr	cag Gln	atg Met	tac Tyr	ata Ile	gat Asp	gat Asp	tta Leu	cca Pro	ata Ile	tgg Trp	383
			115					120					125			
ggt Gly	att Ile	gtt Val	ggt Gly	gag Glu	gct Ala	gat Asp	gaa Glu	aat Asn	gga Gly	gaa Glu	gat Asp	tac Tyr	tat Tyr	ctt Leu	tgg Trp	431
		130					135					140				
acc Thr	tat Tyr	aaa Lys	aaa Lys	ctt Leu	gaa Glu	ata Ile	ggt Gly	ttt Phe	aat Asn	gga Gly	aat Asn	cga Arg	att Ile	gtt Val	gat Asp	479
		145					150					155				
gtt Val	aat Asn	cta Leu	act Thr	agt Ser	gaa Glu	gga Gly	aag Lys	gtg Val	aaa Lys	ctg Leu	gtt Val	cca Pro	aat Asn	act Thr	aaa Lys	527
		160				165				170					175	
atc Ile	cag Gln	atg Met	tca Ser	tat Tyr	tca Ser	gta Val	aaa Lys	tgg Trp	aaa Lys	aag Lys	tca Ser	gat Asp	gtg Val	aaa Lys	ttt Phe	575
				180					185					190		
gaa Glu	gat Asp	cga Arg	ttt Phe	gac Asp	aaa Lys	tat Tyr	ctt Leu	gat Asp	ccg Pro	tcc Ser	ttt Phe	ttt Phe	caa Gln	cat His	cgg Arg	623
			195					200					205			
att Ile	cat His	tgg Trp	ttt Phe	tca Ser	att Ile	ttc Phe	aac Asn	tcc Ser	ttc Phe	atg Met	atg Met	gtg Val	atc Ile	ttc Phe	ttg Leu	671
		210					215					220				
gtg Val	ggc Gly	tta Leu	gtt Val	tca Ser	atg Met	att Ile	tta Leu	atg Met	aga Arg	aca Thr	tta Leu	aga Arg	aaa Lys	gat Asp	tat Tyr	719
		225				230					235					
gct Ala	cgg Arg	tac Tyr	agt Ser	aaa Lys	gag Glu	gaa Glu	gaa Glu	atg Met	gat Asp	gat Asp	atg Met	gat Asp	aga Arg	gac Asp	cta Leu	767
					245				250						255	
gga Gly	gat Asp	gaa Glu	tat Tyr	gga Gly	tgg Trp	aaa Lys	cag Gln	gtg Val	cat His	gga Gly	gat Asp	gta Val	ttt Phe	aga Arg	cca Pro	815
				260					265					270		
tca Ser	agt Ser	cac His	cca Pro	ctg Leu	ata Ile	ttt Phe	tcc Ser	tct Ser	ctg Leu	att Ile	ggt Gly	tct Ser	gga Gly	tgt Cys	cag Gln	863
			275					280					285			
ata Ile	ttt Phe	gct Ala	gtg Val	tct Ser	ctc Leu	atc Ile	gtt Val	att Ile	att Ile	ggt Val	gca Ala	atg Met	ata Ile	gaa Glu	gat Asp	911
		290					295				300					
tta Leu	tat Tyr	act Thr	gag Glu	agg Arg	gga Gly	tca Ser	atg Met	ctc Leu	agt Ser	aca Thr	gcc Ala	ata Ile	ttt Phe	gtc Val	tat Tyr	959

305	310	315	
gct gct acg tct cca gtg aat ggt tat ttt gga gga agt ctg tat gct Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala 320 325 330 335			1007
aga caa gga gga agg aga tgg ata aag cag atg ttt att ggg gca ttc Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe 340 345 350			1055
ctt atc cca gct atg gtg tgt ggc act gcc ttc ttc atc aat ttc ata Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile 355 360 365			1103
gcc att tat tac cat gct tca aga gcc att cct ttt gga aca atg gtg Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val 370 375 380			1151
gcc gtt tgt tgc atc tgt ttt ttt gtt att ctt cct cta aat ctt gtt Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val 385 390 395			1199
ggt aca ata ctt ggc cga aat ctg tca ggt cag ccc aac ttt cct tgt Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys 400 405 410 415			1247
cgt gtc aat gct gtg cct cgt cct ata ccg gag aaa aaa tgg ttc atg Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met 420 425 430			1295
gag cct gcg gtt att gtt tgc ctg ggt gga att tta cct ttt ggt tca Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser 435 440 445			1343
atc ttt att gaa atg tat ttc atc ttc acg tct ttc tgg gca tat aag Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys 450 455 460			1391
atc tat tat gtc tat ggc ttc atg atg ctg gtg ctg gtt atc ctg tgc Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys 465 470 475			1439
att gtg act gtc tgt gtg act att gtg tgc aca tat ttt cta cta aat Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn 480 485 490 495			1487
gca gaa gat tac cgg tgg caa tgg aca agt ttt ctc tct gct gca tca Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser 500 505 510			1535
act gca atc tat gtt tac atg tat tcc ttt tac tac tat ttt ttc aaa Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys 515 520 525			1583
aca aag atg tat ggc tta ttt caa aca tca ttt tac ttt gga tat atg Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met 530 535 540			1631

gcg gta ttt agc aca gcc ttg ggg ata atg tgt gga gcg att ggt tac 1679
 Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr
 545 550 555

atg gga aca agt gcc ttt gtc cga aaa atc tat act aat gtg aaa att 1727
 Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile
 560 565 570 575

gac tagagaccca agaaaacctg gaactttgga tcaatttctt tttcataggg 1780
 Asp

gtggaacttg cacagcaaaa 1800

<210> 14
 <211> 576
 <212> PRT
 <213> Homo sapiens

<400> 14

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Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp Met
 20 25 30

Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr Phe
 35 40 45

Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His
 50 55 60

Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly
 65 70 75 80

Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu
 85 90 95

Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys
 100 105 110

Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly
 115 120 125

Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr
 130 135 140

Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp Val
 145 150 155 160

Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys Ile
 165 170 175

Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe Glu
 180 185 190

Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg Ile
 195 200 205

His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu Val
 210 215 220

Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala
 225 230 235 240

Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu Gly
 245 250 255

Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro Ser
 260 265 270

Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile
 275 280 285

Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp Leu
 290 295 300

Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr Ala
 305 310 315 320

Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg
 325 330 335

Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe Leu
 340 345 350

Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala
 355 360 365

Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val Ala
 370 375 380

Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val Gly
 385 390 395 400

Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg
 405 410 415

Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met Glu
 420 425 430

Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile
 435 440 445

Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile
 450 455 460

Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile
 465 470 475 480

Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala
 485 490 495

Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr
 500 505 510

Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr
 515 520 525

Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala
 530 535 540

Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr Met
 545 550 555 560

Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp
 565 570 575

<210> 15
 <211> 578
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> SM binding protein

<400> 15

Ala Ala Ala Ala Leu Trp Leu Leu Leu Leu Leu Pro Arg Thr Arg
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Ala Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu
20 25 30

Trp Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys
35 40 45

Tyr Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His
50 55 60

Tyr His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe
65 70 75 80

Ser Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr
85 90 95

Cys Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala
100 105 110

Ile Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile
115 120 125

Trp Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu
130 135 140

Trp Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val
145 150 155 160

Asp Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr
165 170 175

Lys Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys
180 185 190

Phe Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His

195	200	205
Arg Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe 210 215 220		
Leu Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp 225 230 235 240		
Tyr Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp 245 250 255		
Leu Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg 260 265 270		
Pro Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys 275 280 285		
Gln Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu 290 295 300		
Asp Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val 305 310 315 320		
Tyr Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr 325 330 335		
Ala Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala 340 345 350		
Phe Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe 355 360 365		
Ile Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met 370 375 380		
Val Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu 385 390 395 400		
Val Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro 405 410 415		
Cys Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe 420 425 430		

Met Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly
435 440 445

Ser Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr
450 455 460

Lys Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu
465 470 475 480

Cys Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu
485 490 495

Asn Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala
500 505 510

Ser Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe
515 520 525

Lys Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr
530 535 540

Met Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly
545 550 555 560

Tyr Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys
565 570 575

Ile Asp

<210> 16
<211> 589
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<223> endomembrane protein 70

<400> 16

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Ser Leu Leu Thr Pro Thr Phe Ala Ser Asp Ser Asp His Lys Tyr Gln
 20 25 30

Ala Glu Glu Gln Val Thr Leu Trp Val Asn Lys Val Gly Pro Tyr Asn
 35 40 45

Asn Pro Gln Glu Thr Tyr Asn Tyr Tyr Ser Leu Pro Phe Cys Arg Pro
 50 55 60

Ser Gly Asn Asn Val His Lys Trp Gly Gly Leu Gly Glu Val Leu Gly
 65 70 75 80

Gly Asn Glu Leu Ile Asp Ser Glu Ile Ala Ile Lys Phe Met Lys Asn
 85 90 95

Val Glu Arg Ser Val Ile Cys Pro Leu Glu Leu Asp Glu Ala Lys Val
 100 105 110

Lys His Phe Lys Asp Ala Ile Glu Ser Ser Tyr Trp Phe Glu Phe Phe
 115 120 125

Met Gly Met Phe His Val Cys Cys Phe Val Gly Glu Leu His Pro Asp
 130 135 140

Lys Asn Ser Glu Asn Gly Lys His Val Leu Tyr Thr His Lys Asn Ile
 145 150 155 160

Val Val Lys Tyr Asn Lys Asp Gln Ile Ile His Val Asn Leu Thr Gln
 165 170 175

Asp Asn Pro Arg Pro Leu Glu Ala Gly Lys Lys Met Asp Leu Thr Tyr
 180 185 190

Ser Val Gln Trp Ile Pro Thr Asn Val Thr Phe Ala Arg Arg Phe Asp
 195 200 205

Val Tyr Leu Asp Tyr Pro Phe Phe Glu His Gln Ile His Trp Phe Ser
 210 215 220

Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu Thr Gly Leu Val Ser
 225 230 235 240

Met Ile Leu Met Arg Thr Leu Arg Asn Asp Tyr Ala Lys Tyr Ala Arg
 245 250 255

Glu Asp Asp Asp Leu Glu Ser Leu Glu Arg Asp Val Ser Glu Glu Ser
 260 265 270

Gly Trp Lys Leu Val His Gly Asp Val Phe Arg Pro Ala Ser Ser Leu
 275 280 285

Val Leu Leu Ser Ala Val Val Gly Thr Gly Ala Gln Leu Ala Leu Leu
 290 295 300

Val Leu Leu Val Ile Leu Met Ala Ile Val Gly Thr Leu Tyr Val Gly
 305 310 315 320

Arg Gly Ala Ile Val Thr Thr Phe Ile Val Cys Tyr Ala Leu Thr Ser
 325 330 335

Phe Val Ser Gly Tyr Val Ser Gly Gly Met Tyr Ser Arg Ser Gly Gly
 340 345 350

Lys His Trp Ile Lys Cys Met Val Leu Thr Ala Ser Leu Phe Pro Phe
 355 360 365

Leu Cys Phe Gly Ile Gly Phe Leu Leu Asn Thr Ile Ala Ile Phe Tyr
 370 375 380

Gly Ser Leu Ala Ala Ile Pro Phe Gly Thr Met Val Val Val Phe Val
 385 390 395 400

Ile Trp Gly Phe Ile Ser Phe Pro Leu Ala Leu Leu Gly Thr Val Val
 405 410 415

Gly Arg Asn Trp Ser Gly Ala Pro Asn Asn Pro Cys Arg Val Lys Thr
 420 425 430

Ile Pro Arg Pro Ile Pro Glu Lys Lys Trp Tyr Leu Thr Pro Ser Val
 435 440 445

Val Ser Leu Met Gly Gly Leu Leu Pro Phe Gly Ser Ile Phe Ile Glu
 450 455 460

Met Tyr Phe Val Phe Thr Ser Phe Trp Asn Tyr Lys Val Tyr Tyr Val

465 470 475 480

Tyr Gly Phe Met Leu Leu Val Phe Val Ile Leu Val Ile Val Thr Val
485 490 495

Cys Val Thr Ile Val Gly Thr Tyr Phe Leu Leu Asn Ala Glu Asn Tyr
500 505 510

His Trp Gln Trp Thr Ser Phe Phe Ser Ala Ala Ser Thr Ala Val Tyr
515 520 525

Val Tyr Leu Tyr Ser Ile Tyr Tyr Tyr Tyr Val Lys Thr Lys Met Ser
530 535 540

Gly Phe Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Thr Met Met Phe Cys
545 550 555 560

Leu Gly Leu Gly Ile Leu Cys Gly Ala Val Gly Tyr Leu Gly Ser Asn
565 570 575

Leu Phe Val Arg Arg Ile Tyr Arg Asn Ile Lys Cys Asp
580 585

<210> 17
<211> 606
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> transmembrane 9 superfamily, protein member 1 precursor (hMP70)

<400> 17

Met Thr Val Val Gly Asn Pro Arg Ser Trp Ser Cys Gln Trp Leu Pro
1 5 10 15

Ile Leu Ile Leu Leu Leu Gly Thr Gly His Gly Pro Gly Val Glu Gly
20 25 30

Val Thr His Tyr Lys Ala Gly Asp Pro Val Ile Leu Tyr Val Asn Lys
35 40 45

Val Gly Pro Tyr His Asn Pro Gln Glu Thr Tyr His Tyr Tyr Gln Leu
50 55 60

Pro Val Cys Cys Pro Glu Lys Ile Arg His Lys Ser Leu Ser Leu Gly
 65 70 75 80

Glu Val Leu Asp Gly Asp Arg Met Ala Glu Ser Leu Tyr Glu Ile Arg
 85 90 95

Phe Arg Glu Asn Val Glu Lys Arg Ile Leu Cys His Met Gln Leu Ser
 100 105 110

Ser Ala Gln Val Glu Gln Leu Arg Gln Ala Ile Glu Glu Leu Tyr Tyr
 115 120 125

Phe Glu Phe Val Val Asp Asp Leu Pro Ile Arg Gly Phe Val Gly Tyr
 130 135 140

Met Glu Glu Ser Gly Phe Leu Pro His Ser His Lys Ile Gly Leu Trp
 145 150 155 160

Thr His Leu Asp Phe His Leu Glu Phe His Gly Asp Arg Ile Ile Phe
 165 170 175

Ala Asn Val Ser Val Arg Asp Val Lys Pro His Ser Leu Asp Gly Leu
 180 185 190

Arg Pro Asp Glu Phe Leu Gly Leu Thr His Thr Tyr Ser Val Arg Trp
 195 200 205

Ser Glu Thr Ser Val Glu Arg Arg Ser Asp Arg Arg Arg Gly Asp Asp
 210 215 220

Gly Gly Phe Phe Pro Arg Thr Leu Glu Ile His Trp Leu Ser Ile Ile
 225 230 235 240

Asn Ser Met Val Leu Val Phe Leu Leu Val Gly Phe Val Ala Val Ile
 245 250 255

Leu Met Arg Val Leu Arg Asn Asp Leu Ala Arg Tyr Asn Leu Asp Glu
 260 265 270

Glu Thr Thr Ser Ala Gly Ser Gly Asp Asp Phe Asp Gln Gly Asp Asn
 275 280 285

Gly Trp Lys Ile Ile His Thr Asp Val Phe Arg Phe Pro Pro Tyr Arg
 290 295 300

Gly Leu Leu Cys Ala Val Leu Gly Val Gly Ala Gln Phe Leu Ala Leu
 305 310 315 320

Gly Thr Gly Ile Ile Val Met Ala Leu Leu Gly Met Phe Asn Val His
 325 330 335

Arg His Gly Ala Ile Asn Ser Ala Ala Ile Leu Leu Tyr Ala Leu Thr
 340 345 350

Cys Cys Ile Ser Gly Tyr Val Ser Ser His Phe Tyr Arg Gln Ile Gly
 355 360 365

Gly Glu Arg Trp Val Trp Asn Ile Ile Leu Thr Thr Ser Leu Phe Ser
 370 375 380

Val Pro Phe Phe Leu Thr Trp Ser Val Val Asn Ser Val His Trp Ala
 385 390 395 400

Asn Gly Ser Thr Cln Ala Leu Pro Ala Thr Thr Ile Leu Leu Leu Leu
 405 410 415

Thr Val Trp Leu Leu Val Gly Phe Pro Leu Thr Val Ile Gly Gly Ile
 420 425 430

Phe Gly Lys Asn Asn Ala Ser Pro Phe Asp Ala Pro Cys Arg Thr Lys
 435 440 445

Asn Ile Ala Arg Glu Ile Asn Pro Gln Pro Trp Tyr Lys Ser Thr Asp
 450 455 460

Ile His Met Thr Val Gly Gly Phe Leu Pro Phe Ser Ala Ile Ser Val
 465 470 475 480

Glu Leu Tyr Tyr Ile Phe Ala Thr Val Trp Gly Arg Glu Gln Tyr Thr
 485 490 495

Leu Tyr Gly Ile Leu Phe Phe Val Phe Ala Ile Leu Leu Ser Val Gly
 500 505 510

Ala Ser Ile Ser Ile Ala Leu Thr Tyr Phe Gln Leu Ser Gly Glu Asp
515 520 525

Tyr Arg Trp Trp Trp Arg Ser Val Leu Ser Val Gly Ser Thr Gly Leu
530 535 540

Phe Ile Phe Leu Tyr Ser Val Phe Tyr Tyr Ala Arg Arg Ser Asn Met
545 550 555 560

Ser Gly Ala Val Gln Thr Val Glu Phe Phe Gly Tyr Ser Leu Leu Thr
565 570 575

Gly Tyr Val Phe Phe Leu Met Leu Gly Thr Ile Ser Phe Phe Ser Ser
580 585 590

Leu Lys Phe Ile Arg Tyr Ile Tyr Val Asn Leu Lys Met Asp
595 600 605

<210> 18
<211> 662
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> multispanning membrane protein p76

<400> 18

Met Ser Ala Arg Leu Pro Val Leu Ser Pro Pro Arg Trp Pro Arg Leu
1 5 10 15

Leu Leu Leu Ser Leu Leu Leu Leu Gly Ala Val Pro Gly Pro Arg Ser
20 25 30

Gly Ala Phe Tyr Leu Pro Gly Leu Ala Pro Val Asn Phe Cys Asp Glu
35 40 45

Glu Lys Lys Ser Asp Glu Cys Lys Ala Glu Ile Glu Leu Phe Val Asn
50 55 60

Arg Leu Asp Ser Val Glu Ser Val Leu Pro Tyr Glu Tyr Thr Ala Phe
65 70 75 80

Asp Phe Cys Gln Ala Ser Glu Gly Lys Arg Pro Ser Glu Asn Leu Gly

				85				90				95				
Gln	Val	Leu	Phe	Gly	Glu	Arg	Ile	Glu	Pro	Ser	Pro	Tyr	Lys	Phe	Thr	
			100				105						110			
Phe	Asn	Lys	Lys	Glu	Thr	Cys	Lys	Leu	Val	Cys	Thr	Lys	Thr	Tyr	His	
			115				120						125			
Thr	Glu	Lys	Ala	Glu	Asp	Lys	Gln	Lys	Leu	Glu	Phe	Leu	Lys	Lys	Ser	
			130				135						140			
Met	Leu	Leu	Asn	Tyr	Gln	His	His	Trp	Ile	Val	Asp	Asn	Met	Pro	Val	
145				150						155			160			
Thr	Trp	Cys	Tyr	Asp	Val	Glu	Asp	Gly	Gln	Arg	Phe	Cys	Asn	Pro	Gly	
			165						170						175	
Phe	Pro	Ile	Gly	Cys	Tyr	Ile	Thr	Asp	Lys	Gly	His	Ala	Lys	Asp	Ala	
			180				185						190			
Cys	Val	Ile	Ser	Ser	Asp	Phe	His	Glu	Arg	Asp	Thr	Phe	Tyr	Ile	Phe	
			195				200						205			
Asn	His	Val	Asp	Ile	Lys	Ile	Tyr	Tyr	His	Val	Val	Glu	Thr	Gly	Ser	
			210				215						220			
Met	Gly	Ala	Arg	Leu	Val	Ala	Ala	Lys	Leu	Glu	Pro	Lys	Ser	Phe	Lys	
225				230						235			240			
His	Thr	His	Ile	Asp	Lys	Pro	Asp	Cys	Ser	Gly	Pro	Pro	Met	Asp	Ile	
			245						250						255	
Ser	Asn	Lys	Ala	Ser	Gly	Glu	Ile	Lys	Ile	Ala	Tyr	Thr	Tyr	Ser	Val	
			260				265						270			
Ser	Phe	Glu	Glu	Asp	Asp	Lys	Ile	Arg	Trp	Ala	Ser	Arg	Trp	Asp	Tyr	
			275						280						285	
Ile	Leu	Glu	Ser	Met	Pro	His	Thr	His	Ile	Gln	Trp	Phe	Ser	Ile	Met	
			290				295						300			
Asn	Ser	Leu	Val	Ile	Val	Leu	Phe	Leu	Ser	Gly	Met	Val	Ala	Met	Ile	
305				310						315			320			

Met Leu Arg Thr Leu His Lys Asp Ile Ala Arg Tyr Asn Gln Met Asp
325 330 335

Ser Thr Glu Asp Ala Gln Glu Glu Phe Gly Trp Lys Leu Val His Gly
340 345 350

Asp Ile Phe Arg Pro Pro Arg Lys Gly Met Leu Leu Ser Val Phe Leu
355 360 365

Gly Ser Gly Thr Gln Ile Leu Ile Met Thr Phe Val Thr Leu Phe Phe
370 375 380

Ala Cys Leu Gly Phe Leu Ser Pro Ala Asn Arg Gly Ala Leu Met Thr
385 390 395 400

Cys Ala Val Val Leu Trp Val Leu Leu Gly Thr Pro Ala Gly Tyr Val
405 410 415

Ala Ala Arg Phe Tyr Lys Ser Phe Gly Gly Glu Lys Trp Lys Thr Asn
420 425 430

Val Leu Leu Thr Ser Phe Leu Cys Pro Gly Ile Val Phe Ala Asp Phe
435 440 445

Phe Ile Met Asn Leu Ile Leu Trp Gly Glu Gly Ser Ser Ala Ala Ile
450 455 460

Pro Phe Gly Thr Leu Val Ala Ile Leu Ala Leu Trp Phe Cys Ile Ser
465 470 475 480

Val Pro Leu Thr Phe Ile Gly Ala Tyr Phe Gly Phe Lys Lys Asn Ala
485 490 495

Ile Glu His Pro Val Arg Thr Asn Gln Ile Pro Arg Gln Ile Pro Glu
500 505 510

Gln Ser Phe Tyr Thr Lys Pro Leu Pro Gly Ile Ile Met Gly Gly Ile
515 520 525

Leu Pro Phe Gly Cys Ile Phe Ile Gln Leu Phe Phe Ile Leu Asn Ser
530 535 540

Ile Trp Ser His Gln Met Tyr Tyr Met Phe Gly Phe Leu Phe Leu Val
 545 550 555 560

Phe Ile Ile Leu Val Ile Thr Cys Ser Glu Ala Thr Ile Leu Leu Cys
 565 570 575

Tyr Phe His Leu Cys Ala Glu Asp Tyr His Trp Gln Trp Arg Ser Phe
 580 585 590

Leu Thr Ser Gly Phe Thr Ala Val Tyr Phe Leu Ile Tyr Ala Val His
 595 600 605

Tyr Phe Phe Ser Lys Leu Gln Ile Thr Gly Thr Ala Ser Thr Ile Leu
 610 615 620

Tyr Phe Gly Tyr Thr Met Ile Met Val Leu Ile Phe Phe Leu Phe Thr
 625 630 635 640

Gly Thr Ile Gly Phe Phe Ala Cys Phe Trp Phe Val Thr Lys Ile Tyr
 645 650 655

Ser Val Val Lys Val Asp
 660

<210> 19
 <211> 586
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> GenBank No. D87444

<400> 19

Met Arg Pro Leu Pro Gly Ala Leu Gly Val Ala Ala Ala Ala Leu Trp
 1 5 10 15

Leu Leu Leu Leu Leu Leu Pro Arg Thr Arg Ala Asp Glu His Glu His
 20 25 30

Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp Met Asn Thr Val Gly
 35 40 45

Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr Phe Ser Leu Pro Phe
50 55 60

Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His Glu Thr Leu Gly
65 70 75 80

Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly Leu Asp Ile Lys
85 90 95

Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu Ile Asp Leu Asp
100 105 110

Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys Asn His Tyr Trp
115 120 125

Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly Ile Val Gly Glu
130 135 140

Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu
145 150 155 160

Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp Val Asn Leu Thr Ser
165 170 175

Glu Gly Lys Val Lys Leu Gly Ser Lys Tyr Tyr Asn Pro Asp Val Ile
180 185 190

Phe Ser Lys Met Glu Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp
195 200 205

Asn Ile Leu Ile Val Leu Phe Ser His Arg Ile His Trp Phe Ser Ile
210 215 220

Phe Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met
225 230 235 240

Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu
245 250 255

Glu Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp
260 265 270

Lys Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile

275		280		285
Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu	290	295	300	
Ile Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly	305	310	315	320
Ser Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val	325	330	335	
Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg	340	345	350	
Trp Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Gly	355	360	365	
Val His Cys Leu Leu His Gln Phe His Ser His Leu Leu Pro Cys Phe	370	375	380	
Lys Ser His Ser Phe Trp Asn Asn Gly Gly Arg Leu Leu His Leu Phe	385	390	395	400
Phe Cys Tyr Ser Ser Ser Lys Ser Cys Trp Tyr Asn Thr Trp Pro Lys	405	410	415	
Ser Val Arg Ser Ala Gln Leu Ser Leu Ser Cys Gln Cys Cys Ala Ser	420	425	430	
Ser Tyr Thr Gly Glu Lys Met Val His Gly Ala Ala Val Ile Val Cys	435	440	445	
Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe	450	455	460	
Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe	465	470	475	480
Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr	485	490	495	
Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln	500	505	510	

Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met
515 520 525

Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe
530 535 540

Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu
545 550 555 560

Gly Ile Met Cys Gly Ala Ile Gly Tyr Met Gly Thr Ser Ala Phe Val
565 570 575

Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp
580 585

<210> 20
<211> 667
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> Emp70 (p24a 70 kDa precursor)

<400> 20

Met Ile Tyr Lys Met Ala His Val Gln Leu Leu Leu Leu Tyr Phe Phe
1 5 10 15

Val Ser Thr Val Lys Ala Phe Tyr Leu Pro Gly Val Ala Pro Thr Thr
20 25 30

Tyr Arg Glu Asn Asp Asn Ile Pro Leu Leu Val Asn His Leu Thr Pro
35 40 45

Ser Met Asn Tyr Gln His Lys Asp Glu Asp Gly Asn Asn Val Ser Gly
50 55 60

Asp Lys Glu Asn Phe Leu Tyr Ser Tyr Asp Tyr Tyr Tyr Asn Arg Phe
65 70 75 80

His Phe Cys Gln Pro Glu Lys Val Glu Lys Gln Pro Glu Ser Leu Gly
85 90 95

Ser Val Ile Phe Gly Asp Arg Ile Tyr Asn Ser Pro Phe Gln Leu Asn
 100 105 110

Met Leu Gln Glu Lys Glu Cys Glu Ser Leu Cys Lys Thr Val Ile Pro
 115 120 125

Gly Asp Asp Ala Lys Phe Ile Asn Lys Leu Ile Lys Asn Gly Phe Phe
 130 135 140

Gln Asn Trp Leu Ile Asp Gly Leu Pro Ala Ala Arg Glu Val Tyr Asp
 145 150 155 160

Gly Arg Thr Lys Thr Ser Phe Tyr Gly Ala Gly Phe Asn Leu Gly Phe
 165 170 175

Val Gln Val Thr Gln Gly Thr Asp Ile Glu Ala Thr Pro Lys Gly Ala
 180 185 190

Glu Thr Thr Asp Lys Asp Val Glu Leu Glu Thr Arg Asn Asp Cys Asn
 195 200 205

Met Val Lys Thr Tyr Glu Leu Pro Tyr Phe Ala Asn His Phe Asp Ile
 210 215 220

Met Ile Glu Tyr His Asp Arg Gly Glu Gly Asn Tyr Arg Val Val Gly
 225 230 235 240

Val Ile Val Glu Pro Val Ser Ile Lys Arg Ser Ser Pro Gly Thr Cys
 245 250 255

Glu Thr Thr Gly Ser Pro Leu Met Leu Asp Glu Glu Asn Asp Asn Glu
 260 265 270

Val Tyr Phe Thr Tyr Ser Val Lys Phe Asn Glu Ser Ala Thr Ser Trp
 275 280 285

Ala Thr Arg Trp Asp Lys Tyr Leu His Val Tyr Asp Pro Ser Ile Gln
 290 295 300

Trp Phe Ser Leu Ile Asn Phe Ser Leu Val Val Val Leu Leu Ser Ser
 305 310 315 320

Val Val Ile His Ser Leu Leu Arg Ala Leu Lys Ser Asp Phe Ala Arg
325 330 335

Tyr Asn Glu Leu Asn Leu Asp Asp Asp Phe Gln Glu Asp Ser Gly Trp
340 345 350

Lys Leu Asn His Gly Asp Val Phe Arg Ser Pro Ser Gln Ser Leu Thr
355 360 365

Leu Ser Ile Leu Val Gly Ser Gly Val Gln Leu Phe Leu Met Val Thr
370 375 380

Cys Ser Ile Phe Phe Ala Ala Leu Gly Phe Leu Ser Pro Ser Ser Arg
385 390 395 400

Gly Ser Leu Ala Thr Val Met Phe Ile Leu Tyr Ala Leu Phe Gly Phe
405 410 415

Val Gly Ser Tyr Thr Ser Met Gly Ile Tyr Lys Phe Phe Asn Gly Pro
420 425 430

Tyr Trp Lys Ala Asn Leu Ile Leu Thr Pro Leu Leu Val Pro Gly Ala
435 440 445

Ile Leu Leu Ile Ile Ile Ala Leu Asn Phe Phe Leu Met Phe Val His
450 455 460

Ser Ser Gly Val Ile Pro Ala Ser Thr Leu Phe Phe Met Val Phe Leu
465 470 475 480

Trp Phe Leu Phe Ser Ile Pro Ser Ser Phe Ala Gly Ser Leu Ile Ala
485 490 495

Arg Lys Arg Cys His Trp Asp Glu His Pro Thr Lys Thr Asn Gln Ile
500 505 510

Ala Arg Gln Ile Pro Phe Gln Pro Trp Tyr Leu Lys Thr Ile Pro Ala
515 520 525

Thr Leu Ile Ala Gly Ile Phe Pro Phe Gly Ser Ile Ala Val Glu Leu
530 535 540

Tyr Phe Ile Tyr Thr Ser Leu Trp Phe Asn Lys Ile Phe Tyr Met Phe

545 550 555 560

Gly Phe Leu Phe Phe Ser Phe Leu Leu Leu Thr Leu Thr Ser Ser Leu
565 570 575

Val Thr Ile Leu Ile Thr Tyr His Ser Leu Cys Leu Glu Asn Trp Lys
580 585 590

Trp Gln Trp Arg Gly Phe Ile Ile Gly Gly Ala Gly Cys Ala Leu Tyr
595 600 605

Val Phe Ile His Ser Ile Leu Phe Thr Lys Phe Lys Leu Gly Gly Phe
610 615 620

Thr Thr Ile Val Leu Tyr Val Gly Tyr Ser Ser Val Ile Ser Leu Leu
625 630 635 640

Cys Cys Leu Val Thr Gly Ser Ile Gly Phe Ile Ser Ser Met Leu Phe
645 650 655

Val Arg Lys Ile Tyr Ser Ser Ile Lys Val Asp
660 665

<210> 21
<211> 15
<212> PRT
<213> artificial

<220>
<223> N-terminus of ICYP receptor, for generating antibodies
<400> 21

Phe Phe Gln His Arg Ile His Val Phe Ser Ile Phe Asn His Cys
1 5 10 15